N. Johnson
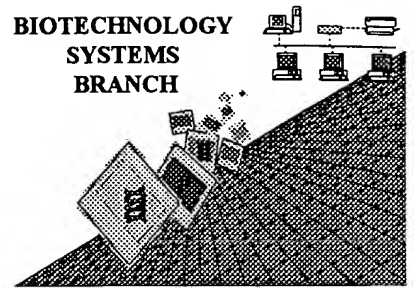
RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: *08/833,506B*

Art Unit / Team No. : *1642*

Date Processed by STIC: *6/14/99*

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u> <u>SUGGESTED CORRECTION</u>   SERIAL NUMBER: _08/833,506B_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(I) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

N. Johnson

1642

INPUT SET: S32213.raw

> This Raw Listing contains the General
> Information Section and those Sequences
> containing ERRORS.

Does Not Comply
Corrected Diskette Needed

```
 1                                    SEQUENCE LISTING
 2
 3    (1)    General Information:
 4    (i)    APPLICANT:  ROBERT WEBBER
 5    (ii)   TITLE OF INVENTION: IMMUNOASSAY METHOD EMPLOYING MONOCLONAL    ANTIBODY REAC
 6    (iii)  NUMBER OF SEQUENCES: 126
 7    (iv)   CORRESPONDENCE ADDRESS:
 8      (A) ADDRESSEE:  BIELEN, PETERSON & LAMPE
 9      (B) STREET:  1990 N. CALIFORNIA BOULEVARD, SUITE 720
10      (C) CITY: WALNUT CREEK
11      (D) STATE: CALIFORNIA
12      (E) COUNTRY: UNITED STATES OF AMERICA
13      (F) ZIP: 94596
14    (v)    COMPUTER READABLE FORM:
15      (A) MEDIUM TYPE:  DISKETTE 3.5 INCH, 1.44 MB FOR FORMATTED
16      (B) COMPUTER: IBM PC COMPATIBLE
17      (C) OPERATING SYSTEM: DOS
18      (D) SOFTWARE: WORDPERFECT 5.1
19    (vi)   CURRENT APPLICATION DATA:
-->20      (A) APPLICATION NUMBER: NONE
21      (B) FILING DATE: NONE
22      (C) CLASSIFICATION:
23    (vii)  PRIOR APPLICATION DATA:
24      (A) APPLICATION NUMBER: 08/634,332
25      (B) FILING DATE: 12 APRIL 1996
26    (viii) ATTORNEY/AGENT INFORMATION:
27      (A) NAME:  THEODORE J. BIELEN, JR.
28      (B) REGISTRATION NUMBER: 27,420
29      (C) REFERENCE/DOCKET NUMBER: 12280
30    (ix)   TELECOMMUNICATION INFORMATION:
31      (A) TELEPHONE: (925) 937-1515
32      (B) TELEFAX:   (925) 937-1529
33
34
```

all text
must be
visible on
page

(see item 3
on Error
summary
sheet)

ERRORED SEQUENCES FOLLOW:

```
   132         (2) INFORMATION FOR SEQ ID NO: 6:
   133    (i) SEQUENCE CHARACTERISTICS:
-->134      (A) LENGTH: 17  18 shown
   135      (B) TYPE: AMINO ACID
   136      (D) TOPOLOGY: LINEAR
```

INPUT SET: S32213.raw

```
137   (ii) MOLECULE TYPE: PEPTIDE
138   (ix) FEATURE:
139    (A) NAME/KEY: MOUSE iNOS (776-792)
140    (B) LOCATION:
141    (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
142    (D) OTHER INFORMATION:
143   (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 6:
144
145   Xaa  Ala  Leu  Val  Gln  Gly  Ile  Leu  Glu  Arg  Val  Val  Asp
146   1                   5    5                    10
147   Cys  Pro  Thr  Pro  His
148        15
149
150
151
```

(misaligned amino acids — see item 4 on Err Summary Sheet)

```
152           (2) INFORMATION FOR SEQ ID NO: 7:
153   (i) SEQUENCE CHARACTERISTICS:
154    (A) LENGTH: (15) 18 shown
155    (B) TYPE: AMINO ACID
156    (D) TOPOLOGY: LINEAR
157   (ii) MOLECULE TYPE: PEPTIDE
158   (ix) FEATURE:
159    (A) NAME/KEY: RAT iNOS (780-794)
160    (B) LOCATION:
161    (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
162    (D) OTHER INFORMATION:
163   (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 7:
164
165   Xaa  Xaa  Leu  Val  Gln  Gly  Ile  Leu  Glu  Arg  Val  Val  Asp
166                       5                        10
167   Cys  Ser  Ser  Pro  Xaa
168        15
169
170
```

```
248           (2) INFORMATION FOR SEQ ID NO: 12:
249   (i) SEQUENCE CHARACTERISTICS:
250    (A) LENGTH: (15) 18 shown
251    (B) TYPE: AMINO ACID
252    (D) TOPOLOGY: LINEAR
253   (ii) MOLECULE TYPE: PEPTIDE
254   (ix) FEATURE:
255       (A) NAME/KEY: HUMAN eNOS (1017-1031)
256       (B) LOCATION:
257       (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
258       (D) OTHER INFORMATION:
259   (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 12:
260
261   Gly  Ile  Ala  Pro  Phe  Arg  Gly  Phe  Trp  Gln  Glu  Arg  Leu
262                       5.                       10
263   His  Asp  Xaa  Xaa  Xaa
264        15
```

PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/833,506B*

DATE: 06/14/1999
TIME: 15:36:13

INPUT SET: S32213.raw

```
        265
        266
─────────────────────────────────────────────────────────────
        267          (2) INFORMATION FOR SEQ ID NO: 13:
        268     (i) SEQUENCE CHARACTERISTICS:
-->     269      (A) LENGTH: (15)   18  ʃʰᵐ
        270      (B) TYPE: AMINO ACID
        271      (D) TOPOLOGY: LINEAR
        272     (ii) MOLECULE TYPE: PEPTIDE
        273     (ix) FEATURE:
        274      (A) NAME/KEY: BOVINE eNOS (1019-1033)
        275      (B) LOCATION:
        276      (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
        277      (D) OTHER INFORMATION:
        278     (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 13:
        279
        280     Gly  Ile  Ala  Pro  Phe  Arg  Gly  Phe  Trp  Gln  Glu  Arg  Leu
        281                         5                        10
        282     His  Asp  Xaa  Xaa  Xaa
        283          15
        284
        285
─────────────────────────────────────────────────────────────
        1524         (2) INFORMATION FOR SEQ ID NO: 82:
        1525    (i) SEQUENCE CHARACTERISTICS:
-->OK   1526     (A) LENGTH: 9
        1527     (B) TYPE: AMINO ACID        ·
        1528     (D) TOPOLOGY: LINEAR
        1529    (ii) MOLECULE TYPE: PEPTIDE
        1530    (ix) FEATURE:
        1531     (A) NAME/KEY: HUMAN iNOS (1009-1017)
        1532     (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
        1533     (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
        1534     (D) OTHER INFORMATION:
        1535    (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 82:
        1536
-->     1537    Arg  Met  Thr  Leu  Val  Phe  Gly  Ser  Arg-amide
        1538    1                   5
        1539
        1540
─────────────────────────────────────────────────────────────
        1541         (2) INFORMATION FOR SEQ ID NO: 83:
        1542    (i) SEQUENCE CHARACTERISTICS:
-->OK   1543     (A) LENGTH: 6
        1544     (B) TYPE: AMINO ACID
        1545     (D) TOPOLOGY: LINEAR
        1546    (ii) MOLECULE TYPE: PEPTIDE
        1547    (ix) FEATURE:
        1548     (A) NAME/KEY: HUMAN iNOS (1009-1014)
        1549     (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
        1550     (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
        1551     (D) OTHER INFORMATION:
        1552    (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 83:
```

delete – do not show this in the sequence itself [handwritten annotation]

```
      1553
-->   1554   Arg  Met  Thr  Leu  Val  Phe-amide   delete
      1555                            5
      1556   1
      1557
      1558
```

```
      2296          (2) INFORMATION FOR SEQ ID NO: 126:
      2297   (i) SEQUENCE CHARACTERISTICS:
      2298    (A) LENGTH: 8
      2299    (B) TYPE: AMINO ACID
      2300    (D) TOPOLOGY: LINEAR
      2301   (ii) MOLECULE TYPE: PEPTIDE
      2302   (ix) FEATURE:
      2303    (A) NAME/KEY: HUMAN iNOS (783-790)
      2304    (B) LOCATION: CARBOXY TERMINAL WITH AMIDE
      2305    (C) IDENTIFICATION METHOD: AMINO ACID ANALYSIS
      2306    (D) OTHER INFORMATION:
      2307
      2308   (xi) SEQUENCE DESCRIPTION:  SEQ ID NO: 126:
      2309
      2310   Leu  Val  Gln  Gly  Ile  Leu  Glu  Arg
      2311                      5
-->   2312   ??
      2313
      2314        delete at
      2315        end of file
      2316
      2317
      2318
      2319
      2320
      2321
      2322
      2323
      2324
      2325
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/833,506B*

INPUT SET: S32213.raw

Line	Error	Original Text
20	Wrong application Serial Number	(A) APPLICATION NUMBER: NONE
134	Entered (17) and Calc. Seq. Length (18) differ	(A) LENGTH: 17
154	Entered (15) and Calc. Seq. Length (18) differ	(A) LENGTH: 15
250	Entered (15) and Calc. Seq. Length (18) differ	(A) LENGTH: 15
269	Entered (15) and Calc. Seq. Length (18) differ	(A) LENGTH: 15
1526	Entered (9) and Calc. Seq. Length (8) differ	(A) LENGTH: 9
1537	Wrong Amino Acid Designator	Arg Met Thr Leu Val Phe Gly Ser Arg-amide
1543	Entered (6) and Calc. Seq. Length (5) differ	(A) LENGTH: 6
1554	Wrong Amino Acid Designator	Arg Met Thr Leu Val Phe-amide
2312	Wrong Amino Acid Designator	??

BIOTECHNOLOGY
SYSTEMS
BRANCH
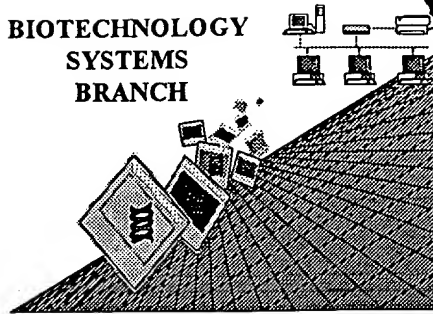
Notice of Availability of Checker Program

Applicant Aid for Biotechnology Computer Readable Form (CRF)
Sequence Listing Submissions

The Patent and Trademark Office (PTO) has developed a computer program, called Checker, that will aid applicants in identifying and correcting errors prior to making submissions for compliance with the Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (Sequence Rules: 37CRF 1.821 through 1.825).
Final rules were published in the *Federal Register* (55 FR18230) on May 1, 1990, and in the PTO *Official Gazette* (1114 Off.Gaz.PatOffice 29) on May 15, 1990.

Checker is a DOS-based software program that is intended to assist users in determining whether errors may be present in the sequence listings, and is not intended to guarantee that the submission is error-free.

The most current version of the software is available via computer downloading, details are below. Copies on diskette are also available. Updated software versions will not be automatically mailed out; any updates will be announced in the PTO *Official Gazette.*

The software can be accessed/requested from the following locations:

1) Dial-up access through the Internet. Location is ftp://ftp.uspto.gov
   The software is in current directory: pub/checker/
   Download all the files. Cost: Free-of-charge

3) For diskette copies, mail to: U.S.P.T.O., OEIP, CRYSTAL PARK 3, SUITE 441
   WASHINGTON DC 20231

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For Further Information, Contact: **Arti Shah at 703-308-4212**